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Fig. 1

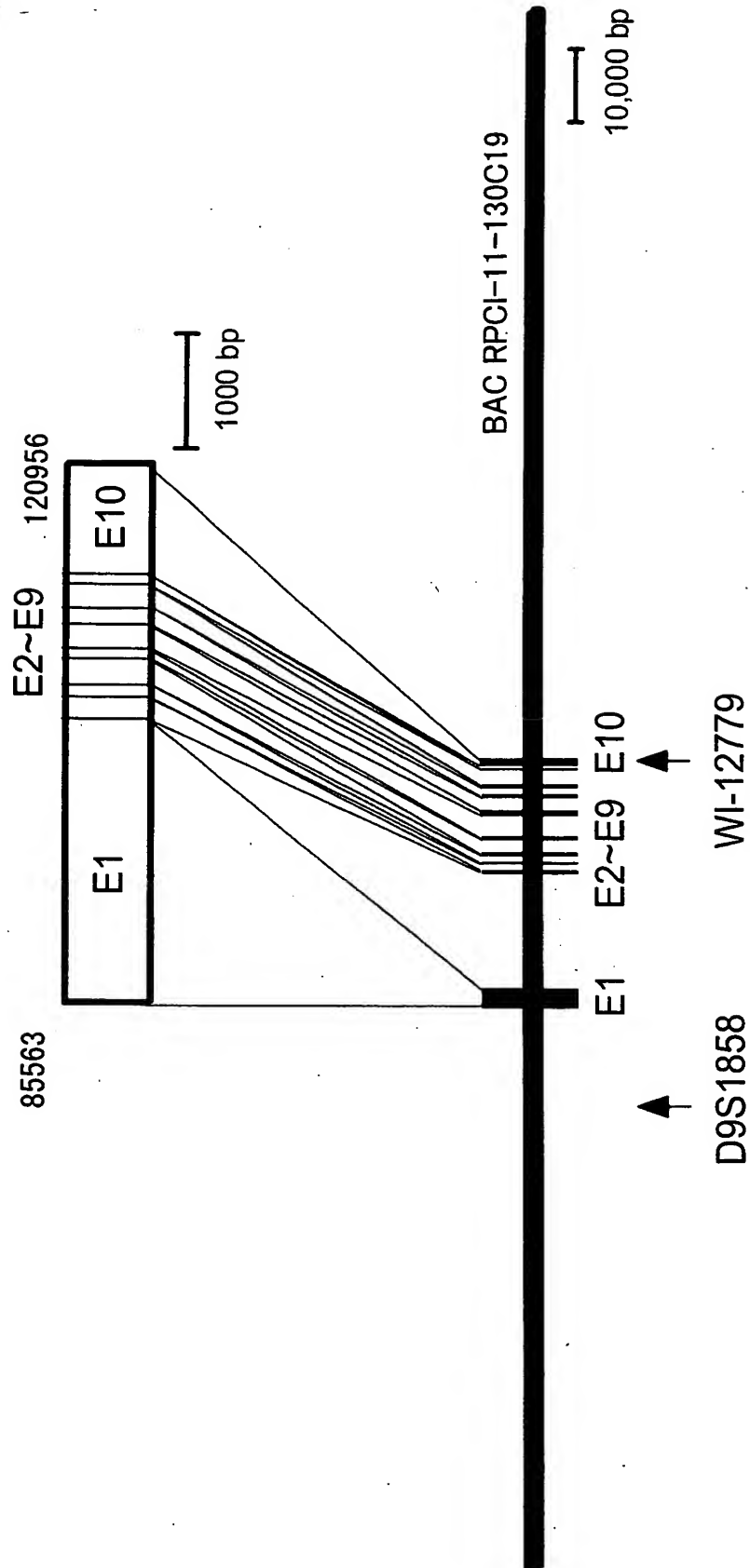
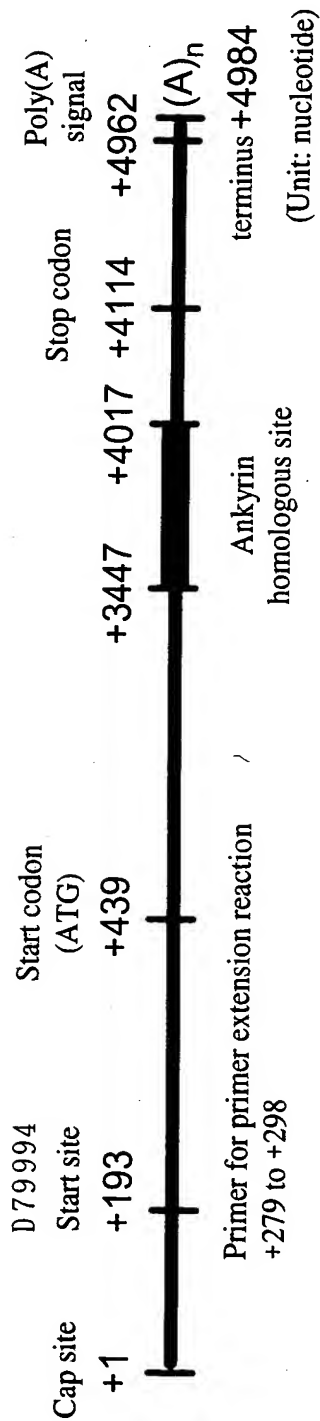
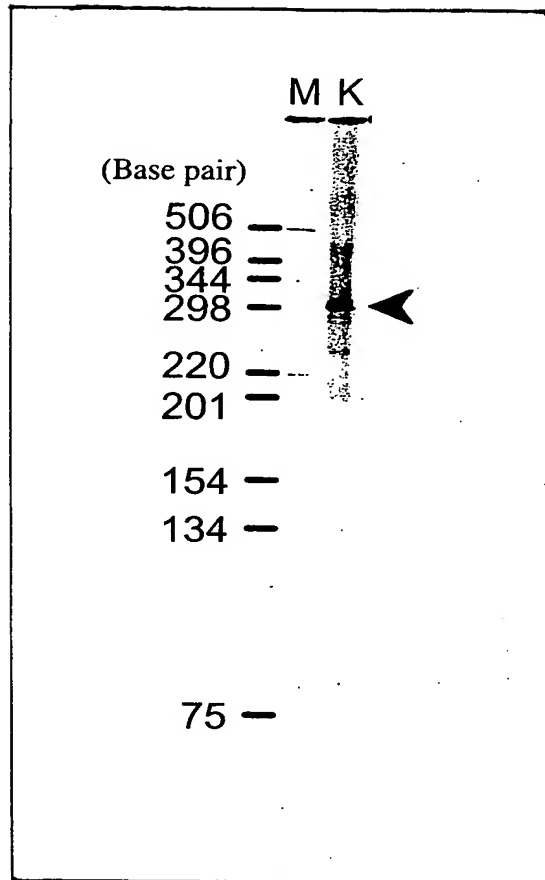


Fig. 2A



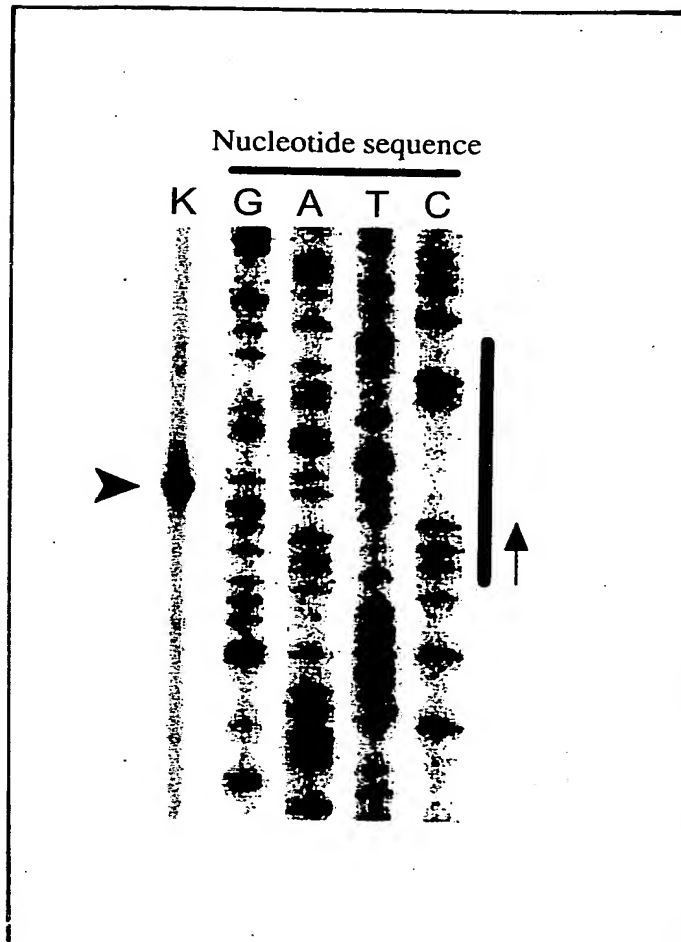
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Fig. 2B



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Fig. 2C



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Fig. 2D

AAAACATAGGTGTGTCAACTCTTAAAATCATACCAGCTTGCTGTA
TTTTGTATCCACACAGTTGAGAATTTTAGTATGGTCGAACGACAT

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Fig. 3

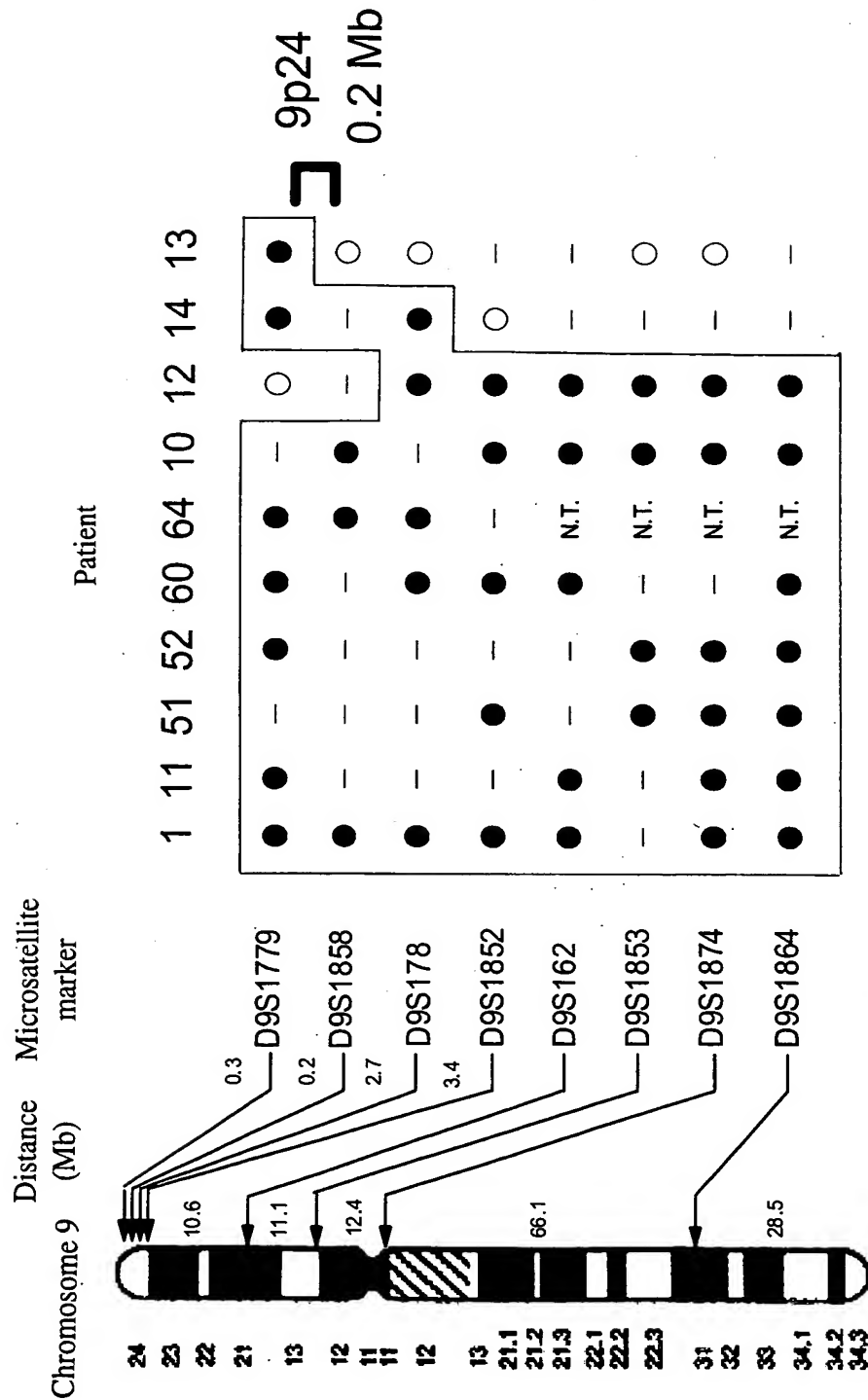
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EIELQQQTIEALKEKIYRLEVQLRETHDREMTKLKQELQAAGSRKKVDKATMAQPLVF
SKVVEAVVQTRDQWVGSHMDLVDTCVGTSVETNSVGISQCECKNKVVGPELPMNWWIV
KERVEMHDCAGRSVEMCDKSVSVESVCETGNTSESVNDLTLLKTNLNLKEVRSIGC
GDCSVDVTVCSPKECASRGVNTAEVQVEAAVMAVPRTADQTDSTDLQVHQFTNTETA
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DRPSAVTKESGVGININDNYLVGLKMRTIACGPPQLTVGLTASRRSVGVGDDDPVGES
LENPQPAPLGMMTGLDHYIERIQKLLAEQQTLAENYSELAFAFEPHSQMSGSLNSQL
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EQEVGTSEGKPISSLDAPFTQEGTLPVNLTDQIAAGLYACTNNESTLKSIMKKKDG
KDSNGAKKNLQFVGINGGYETTSSDDSSDESSSESDECDVIEYPLEEEEEEEDEDT
RGMAEGHHAVNIEGLKSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
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GN

TALHYSVSHSNFEIVKLLLDADVNCVDHQNKAGTPIMLAALAAVEAEKDMRIVEELFG
CGDVNAKASQAGQTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHGHVE
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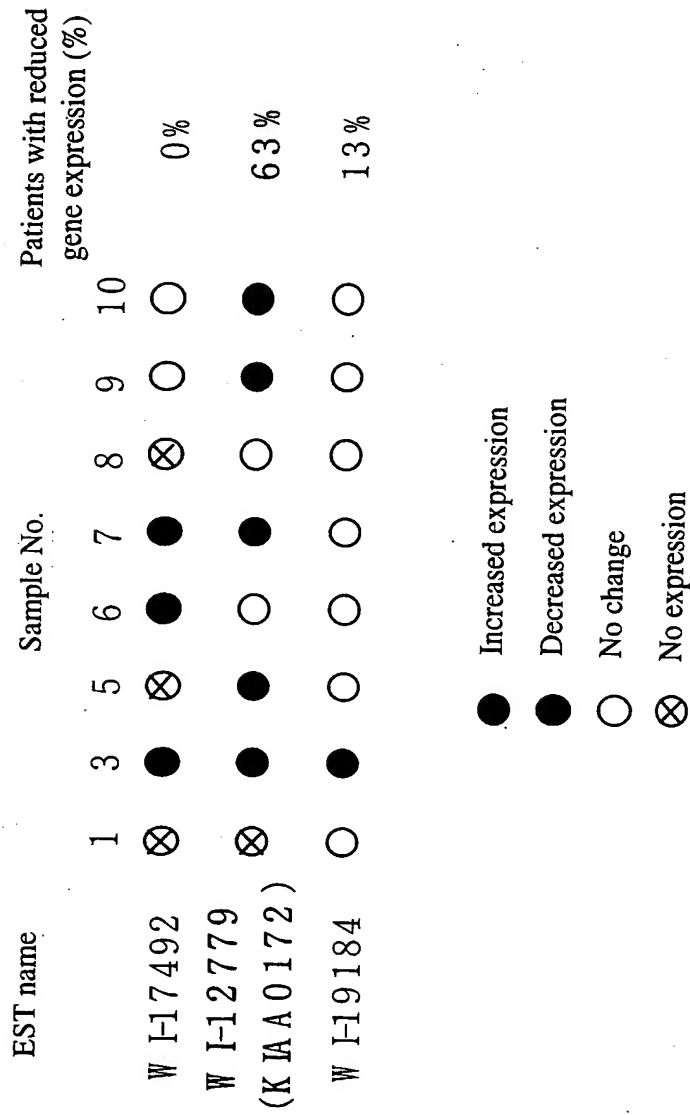
Ankyrin homologous site
1006-1162

Fig. 4



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Fig. 5



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Fig. 6

Codon No.	D79994	Mutation	Change in amino acid	Patient No.	Frequency (%)
52	CAC	CAG	His→Gln	56	1/75 (1.3)
168	GCG	GTG	Ala→Val	4	1/75 (1.3)
268-269	(6 nucleotides inserted)	+GCTGTA	(Ala-Val) Inserted	64	1/75 (1.3)
269	GTA	GGA	Val→Gly	90	1/75 (1.3)
274	GAG	CAG	Glu→Gln	8, 23, 49, 52, 87, 90, 92	7/75 (9.3)
306	TCC	GCC	Ser→Ala	4, 22, 68, 84, 86	5/75 (6.7)
506	GCA	GTA	Ala→Val	15, 83	2/75 (2.6)
509	CGT	CAT	Arg→His	4, 22, 41, 48, 51, 68, 84, 86	8/75 (10.6)
Total				19/75	(25.3)

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Fig. 7

Codon No.	Amino acid	GenBank Data	SNP	Patient No.	Frequency (%)
273	Val	GTT	GTG	11	1.3
299	Leu	CTG	CTC	4, 22, 51, 64, 60, 11, 66, 16, 17, 19	13.3
372	His	CAC	TAC	64	1.3
380	Val	GTT	GTG	42	1.3
497	Val	GTT	GTG	51	3.5
453	Asn	AAC	AAT	16, 21, 52, 8, 23, 41, 49, 51, 67, 68, 84, 86, 89, 91	18.6
478	Asp	GAC	GAT	4, 22, 41, 48, 51, 68, 84, 86	10.7
507	Val	GTG	GTT	66, 16	2.6
1003	Asn	AAC	AAT	10	1.3
1120	Gly	GGG	GGC	12	1.3

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Fig. 8

Patient No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	
LOH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Mutation	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	
SNP																								

○ : No LOH
● : LOH
● : Mutation positive
● : SNP positive

Patient No.	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66
LOH	○	-	-	○	-	○	-	○	-	○	-	●	-	-	-	-	○	○	○	●	-	-	-	●	○	○
	○	-	-	-	-	-	-	○	-	-	-	-	-	○	-	-	○	○	○	-	-	-	○	●	○	○
Mutation	●						●	●	●	●	●	●				●							●	●	○	○
SNP	●	●					●	●	●		●	●							●					●	●	●

Patient No.	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	Frequency
LOH																											6/49 (27.3%)
Mutation																											4/49 (14.3%)
SNP																											19/75 (25.3%)
																											26/75 (34.7%)

Fig. 9

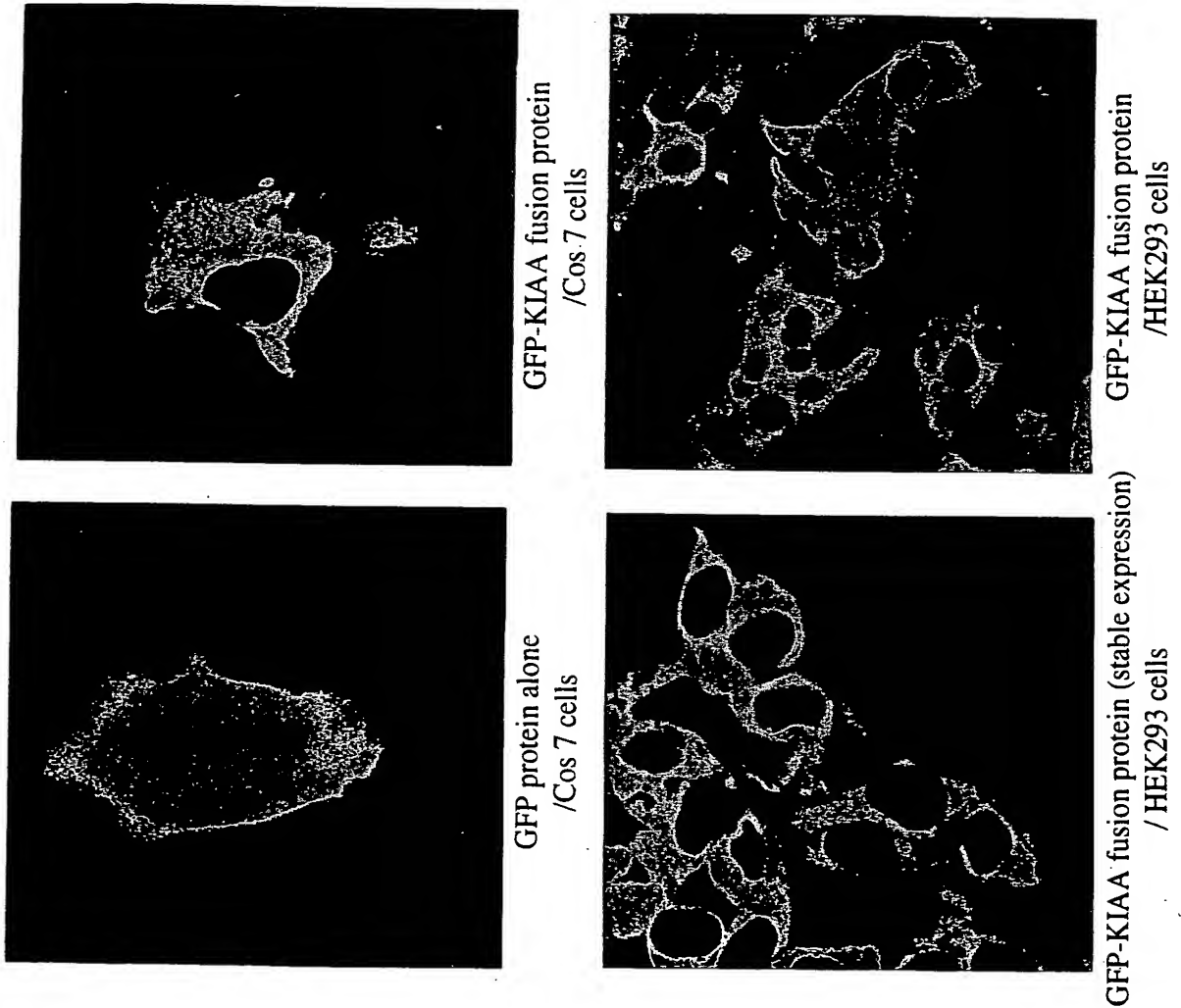
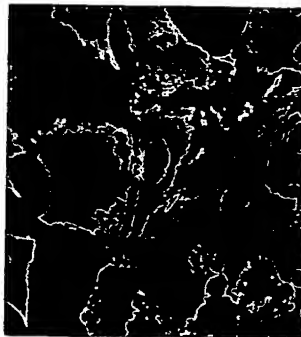


Fig. 10A

Results of immunostaining using an anti-KIAA0172 antibody



Results of staining of
VMRC-RCW cells



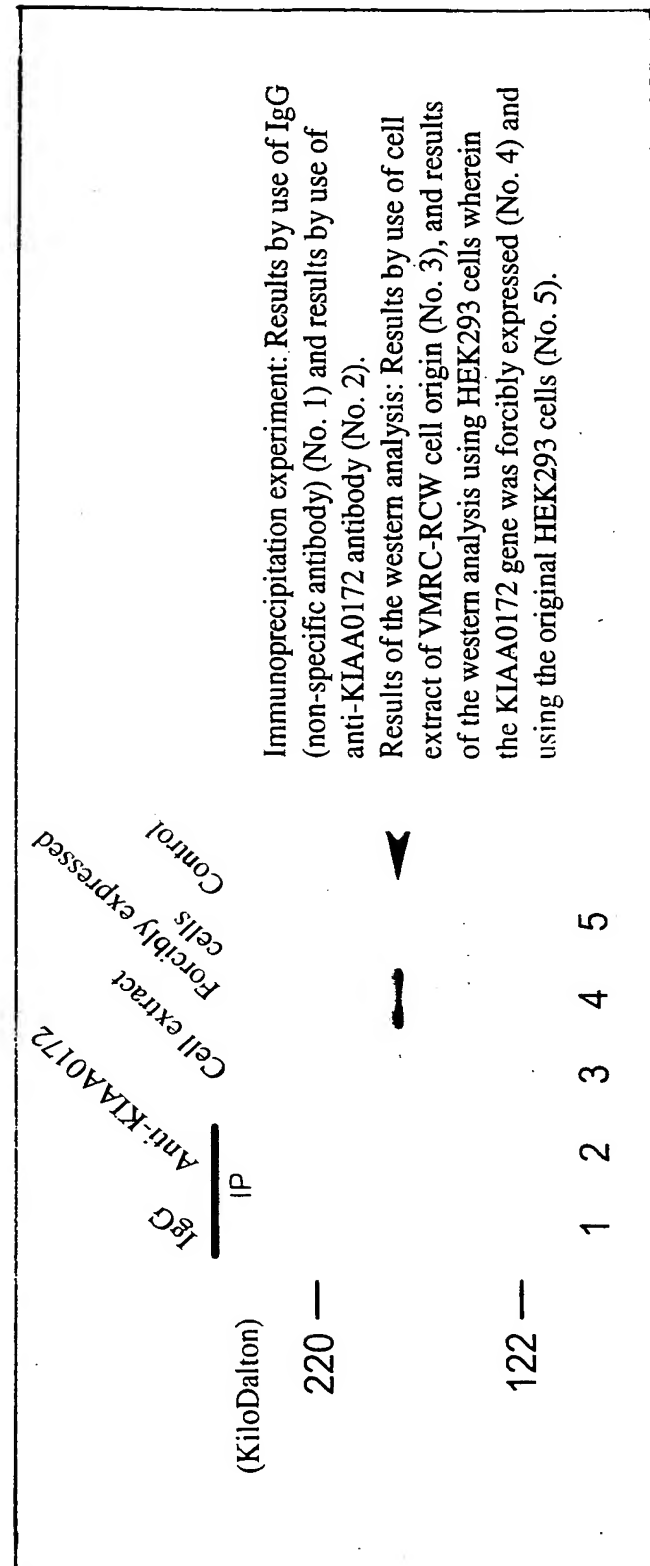
Results of staining of
VMRC-RCW cells
with the antigen added



Results of staining of
HEK293 cells in which KIAA0172
gene was forcibly expressed

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Fig. 10B



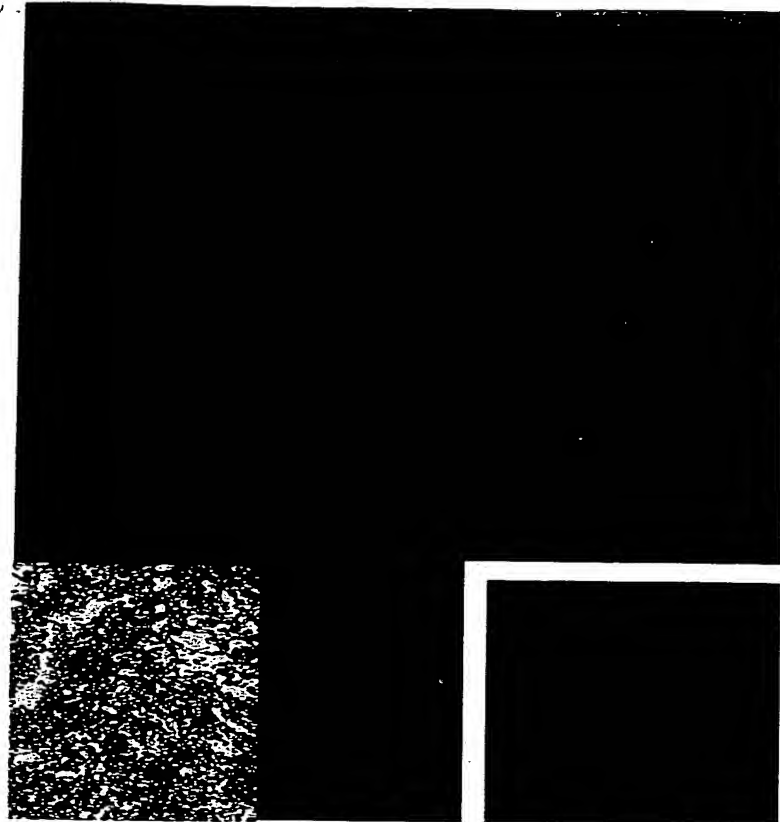
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Fig. 11

Normal tissue



Cancer tissue



Upper left shows the result of HE staining and
lower left is an enlarged view, respectively

Fig. 12A

Result of allele loss in the cancer tissue DNA in gene scan analysis

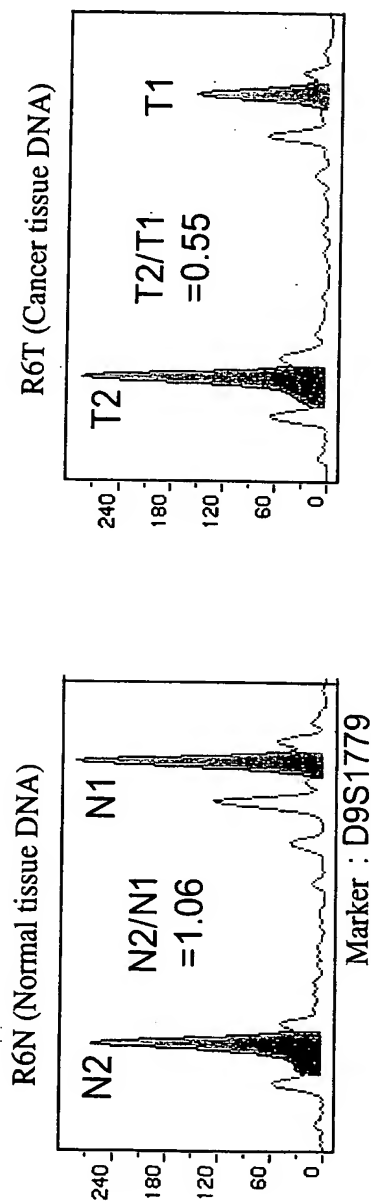


Fig. 12B

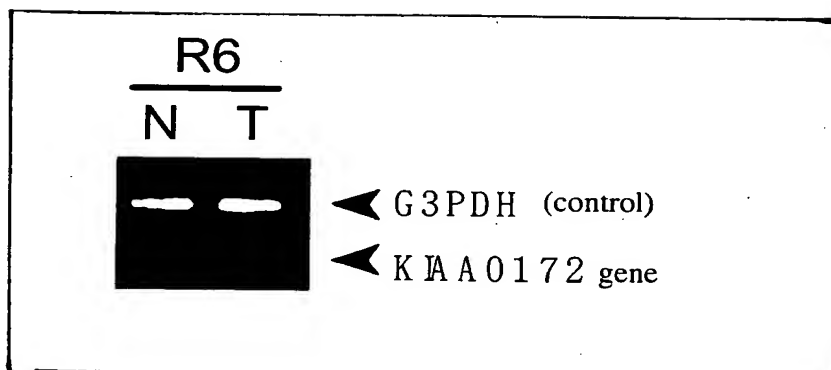
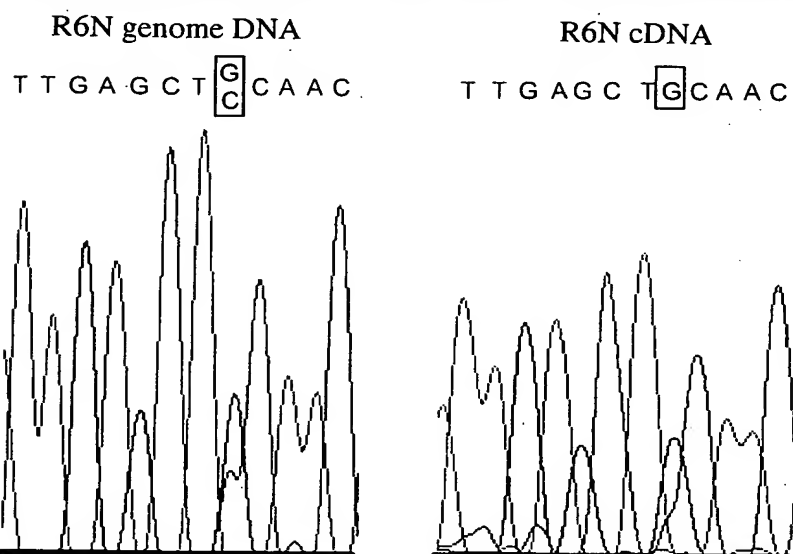


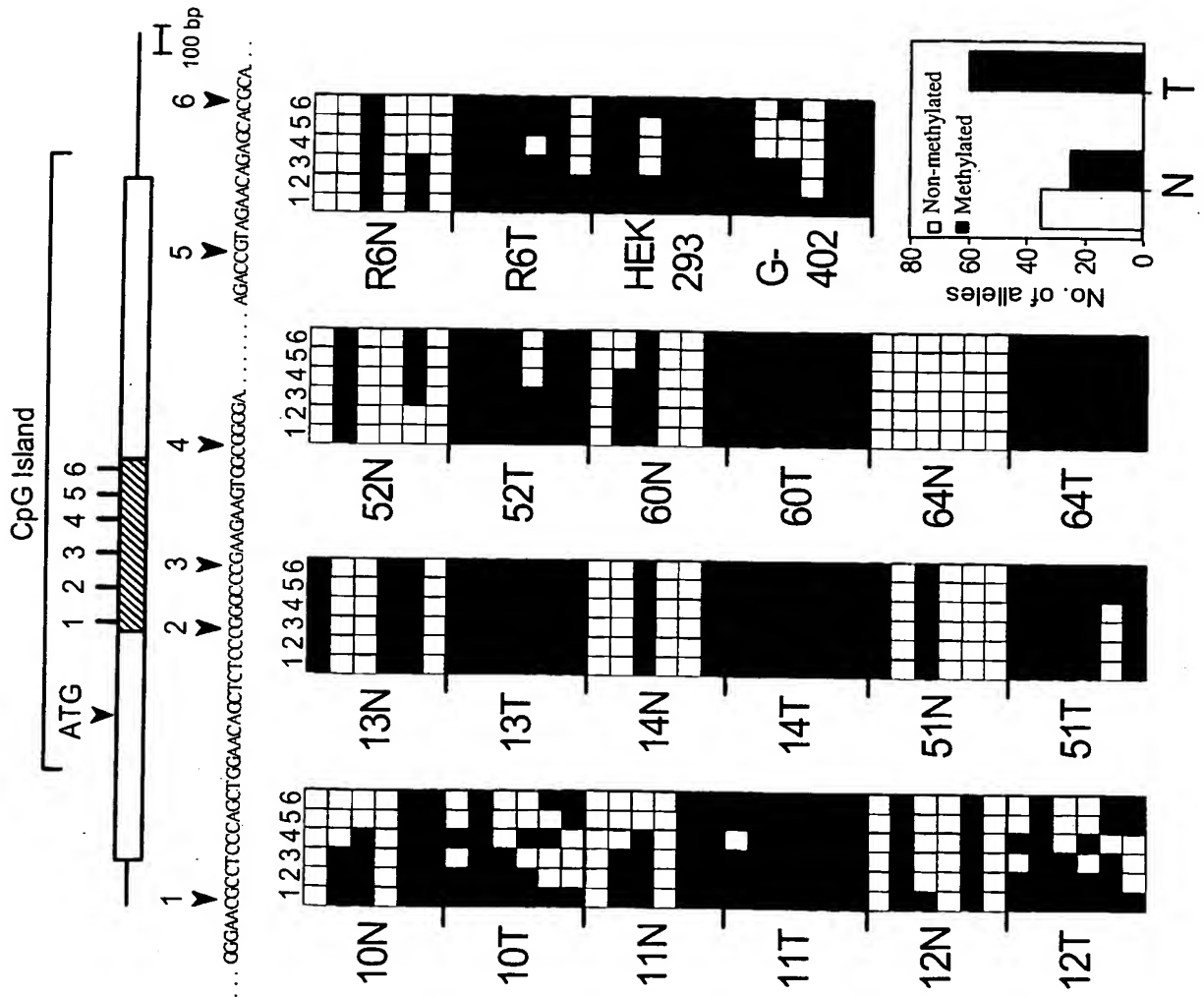
Fig. 12C

Result of allele-specific expression using single nucleotide polymorphism



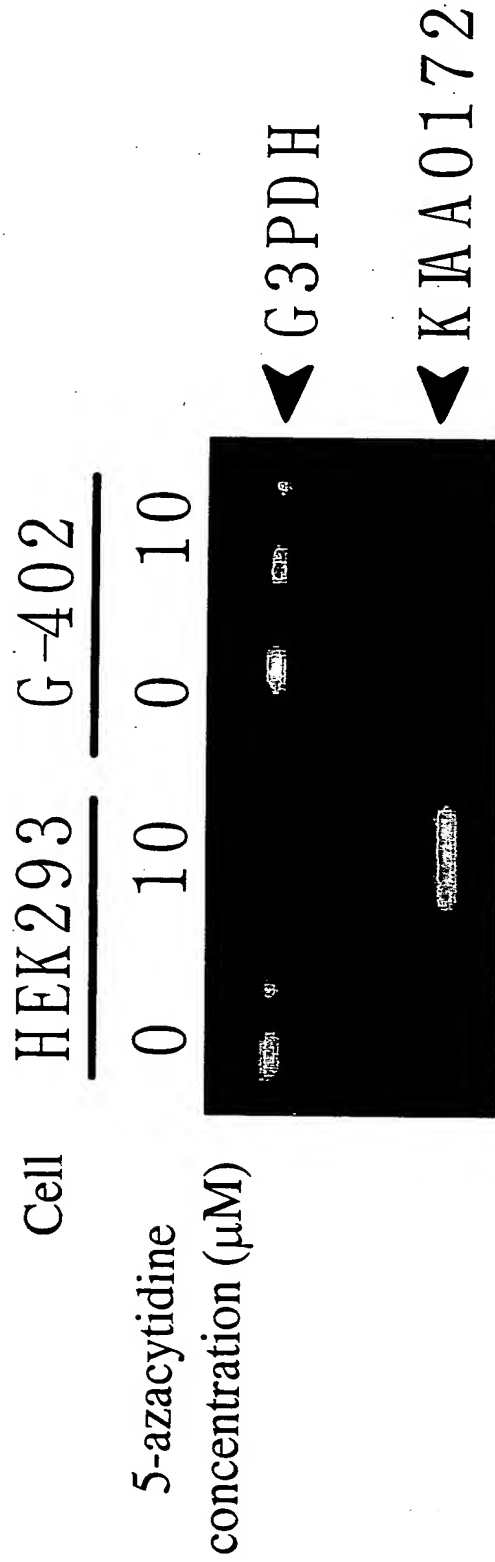
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Fig. 13



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Fig. 14



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Fig. 15A

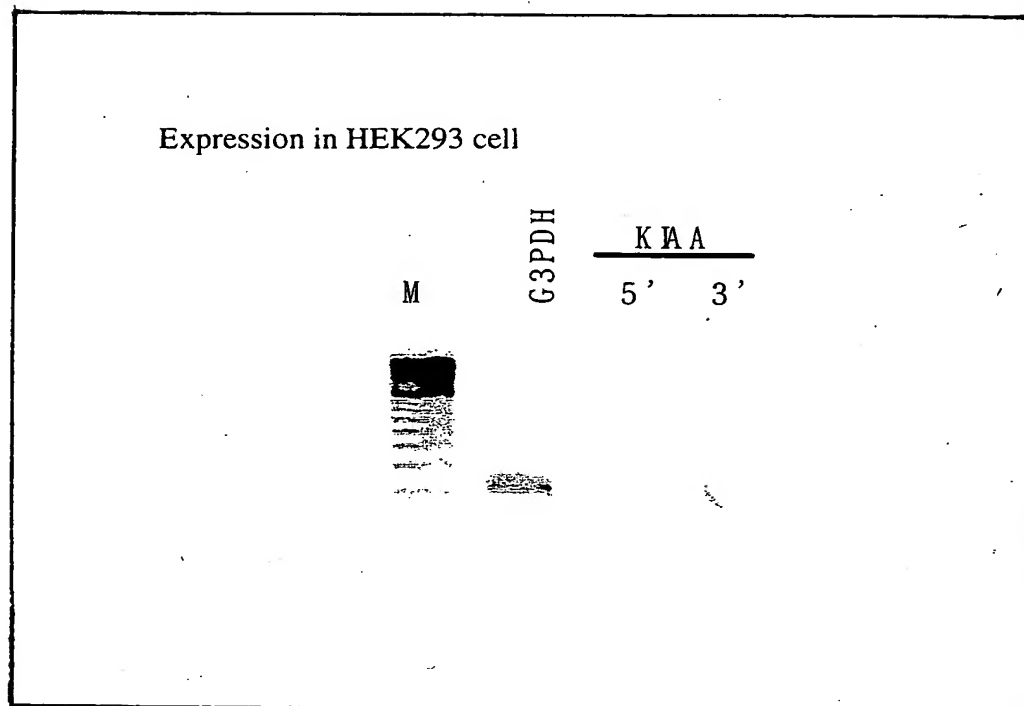
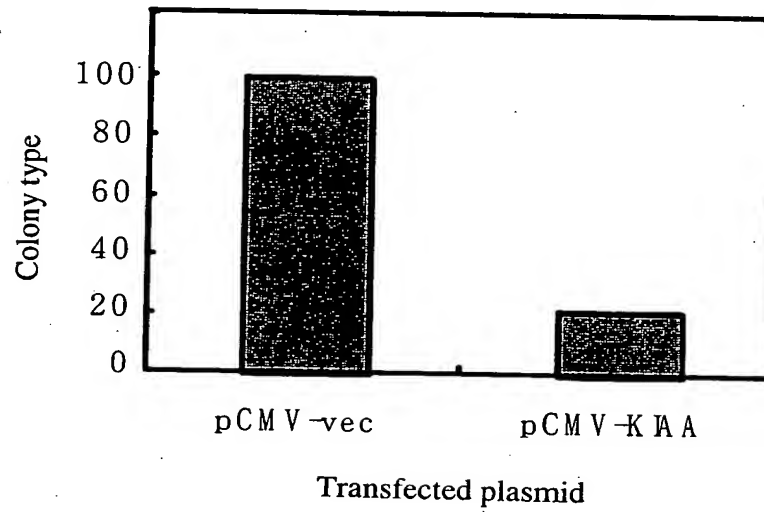


Fig. 15B

Cell proliferation suppressing ability when transfected into HEK293 cell



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Fig. 16A

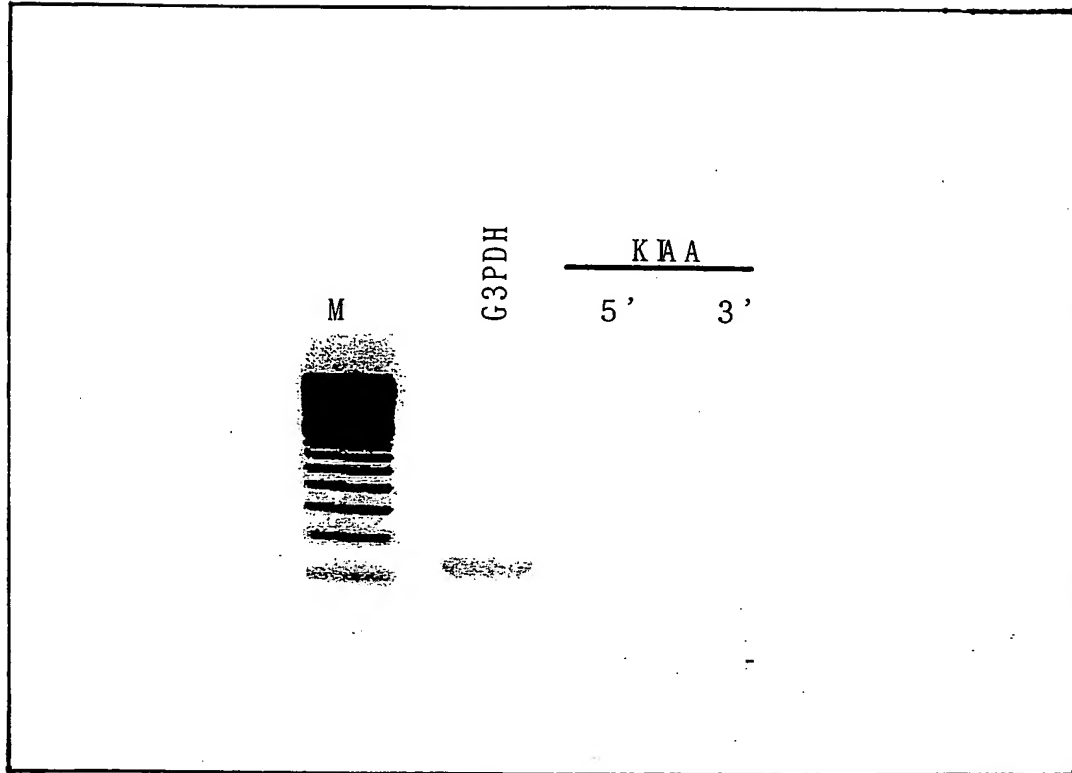
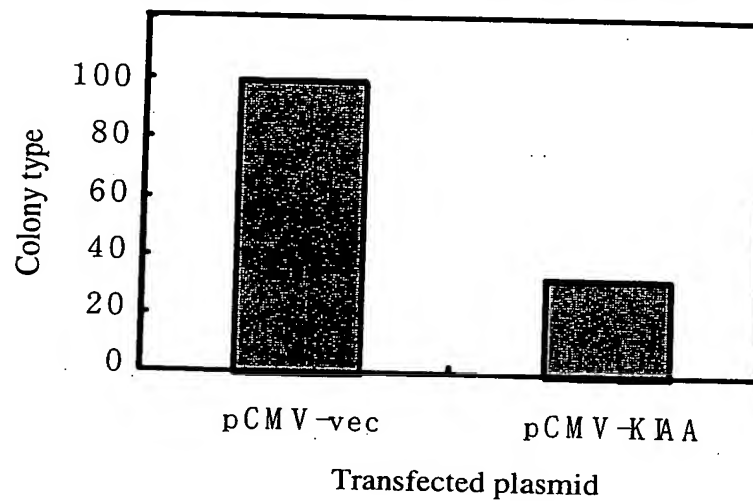


Fig. 16B

Cell proliferation suppressing ability when transfected into G-402 cell



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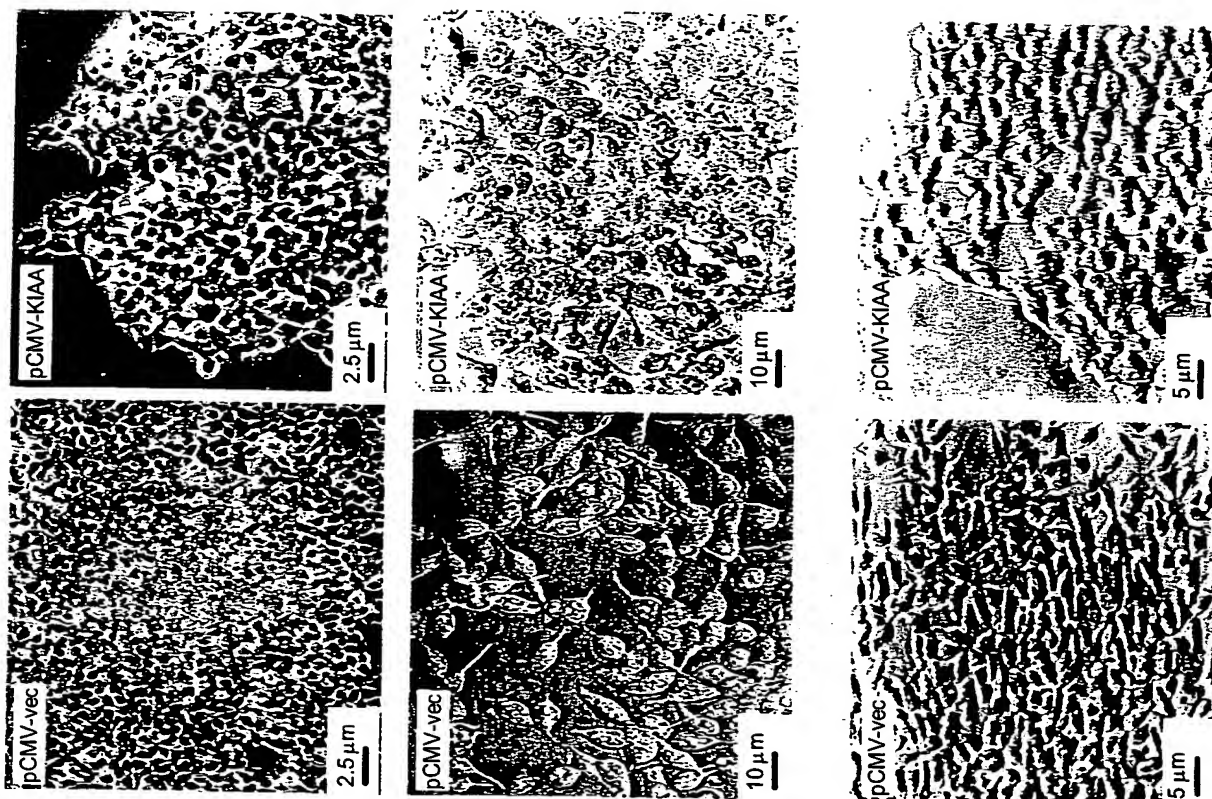
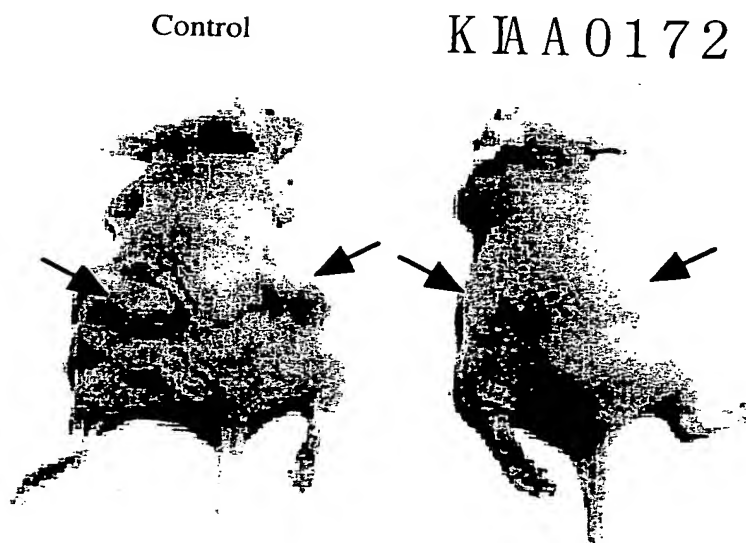


Fig. 17

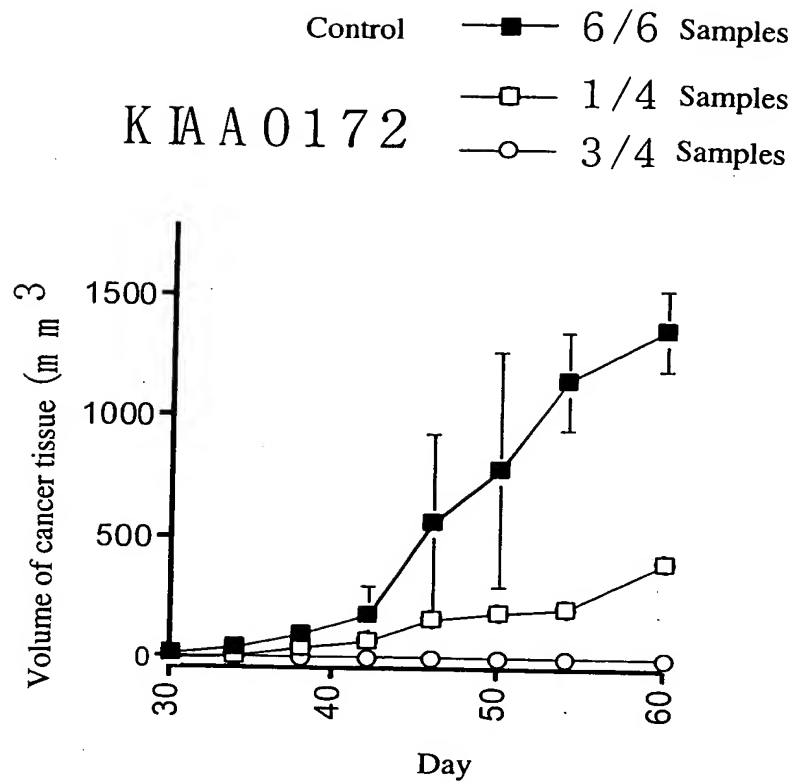
Fig. 18A

Results of experiments where HEK293 cells expressing vector (control) and HEK293 cells expressing KIAA0172 gene were transplanted into abdominal cavity, respectively



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Fig. 18B



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